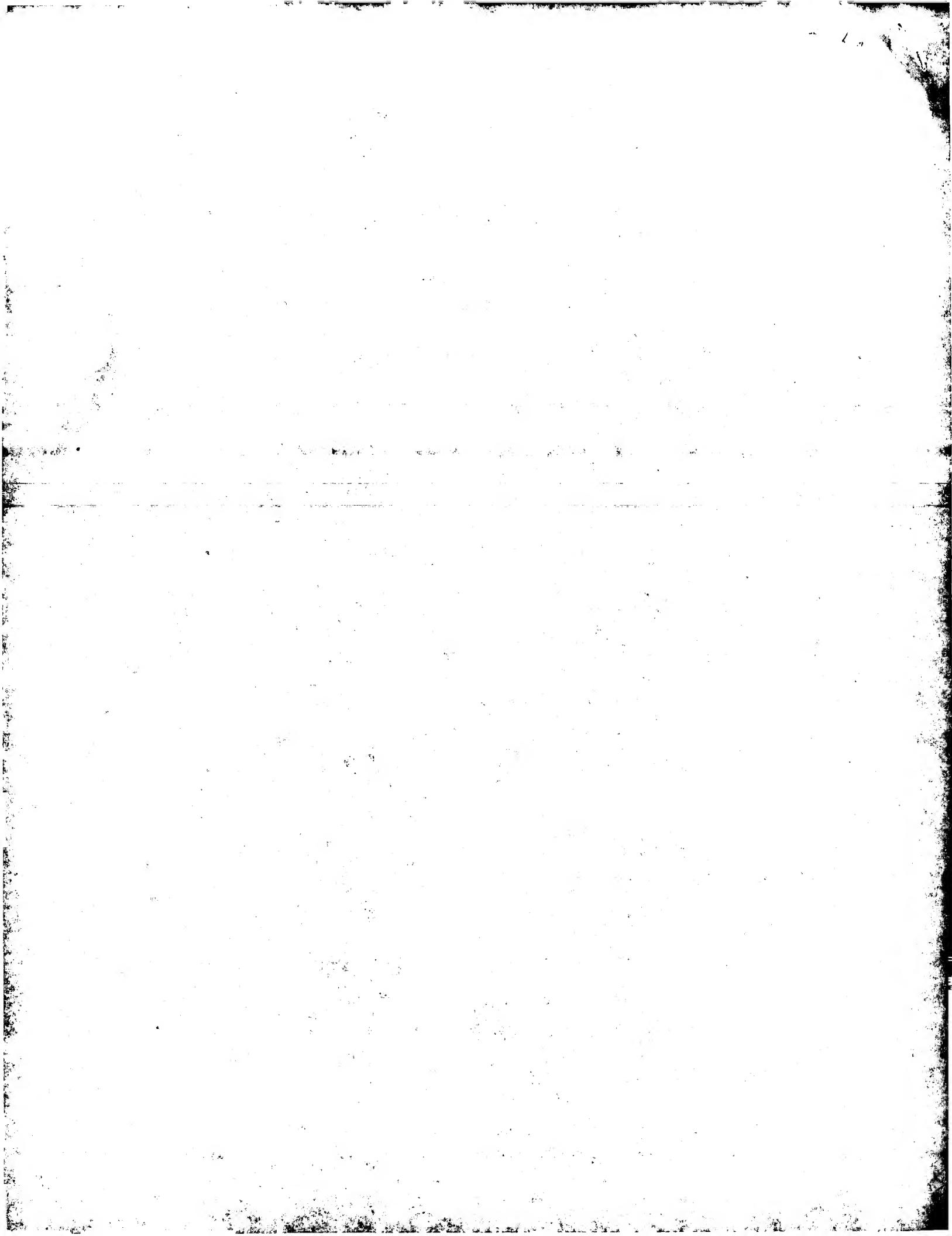


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 DEFINITION Homo sapiens mRNA; cDNA DKF2p586B1922 (from clone DKF2p586B1922).
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 VERSION AL049450.1
 KEYWORDS
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Koehler,K., Beyer,A., Mewes,H.W., Gassnerhuber,J. and Wiemann,S.
 TITLE Direct Submission
 JOURNAL Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152
 COMMENT
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: S.wiemann@dkfz-heidelberg.de;
 sequenced by BMFZ (Biomedical Research Center at the Charite',
 Berlin/Germany) within the cDNA sequencing consortium of the German
 Genome Project.
 This clone (DKF2p586B1922) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
 information about the clone and the sequencing project is available
 at <http://www.mips.biochem.mpg.de/proj/cDNA/>.
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2003, 13:29:30 ; Search time 3 Seconds
 (without alignments)
 4.177 Million cell updates/sec

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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 4372 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1 summaries

Database : US10054935.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
 US-10-054-935-1
 Sequence 1, Application US/10054935
 GENERAL INFORMATION:
 APPLICANT: Oligene Technologies, Inc
 TITLE OF INVENTION: BREAST CANCER TRANSCRIPTION FACTOR GENE AND USES
 FILE REFERENCE: 16U 107 R1
 CURRENT APPLICATION NUMBER: US/10/054,935
 CURRENT FILING DATE: 2002-01-25
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 4372
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (78)..(922)
 OTHER INFORMATION:
 US-10-054-935-1

Query Match 26.5% ; Score 380.2; DB 1; Length 4372;
 Best Local Similarity 95.6% ; Pred. No. 0; Mismatches 18; Indels 0; Gaps 0;
 Matches 391; Conservative 0; Other 0;

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1 mRNA-SEQUENCE 1.0
 LOCUS HSM00235 1433 bp mRNA linear PRI 18-FEB-2000
 DEFINITION Homo sapiens mRNA; cDNA DKFZp586B1922 (from clone DKFZp586B1922).
 ACCESSION AL049450
 VERSION AL049450.1 GI:4500236
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1433)
 AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
 COMMENT DIRECT Submission
 Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152
 Martinsried, GERMANY
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by BMFZ (Biomedical Research Center at the Charite', German
 Genome Project).
 This clone (DKFZp586B1922) is available at the RZPD in Berlin.
 Please contact the RZPD, Ressourcenzentrum, Heinbergsweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
 information about the clone and the sequencing project is available
 at <http://www.mips.biochem.mpg.de/proj/CDNA/>.
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2003, 13:29:30 : search time 3 seconds
(without alignments)
4.177 Million cell updates/sec

Title: HSM000235
Perfect score: 1433
Sequence: 1 TGGAAAGAGCCCTAACAC. ACAAAAAAAAGAAAAA 1433

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 4372 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : US10054935.seq:*

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

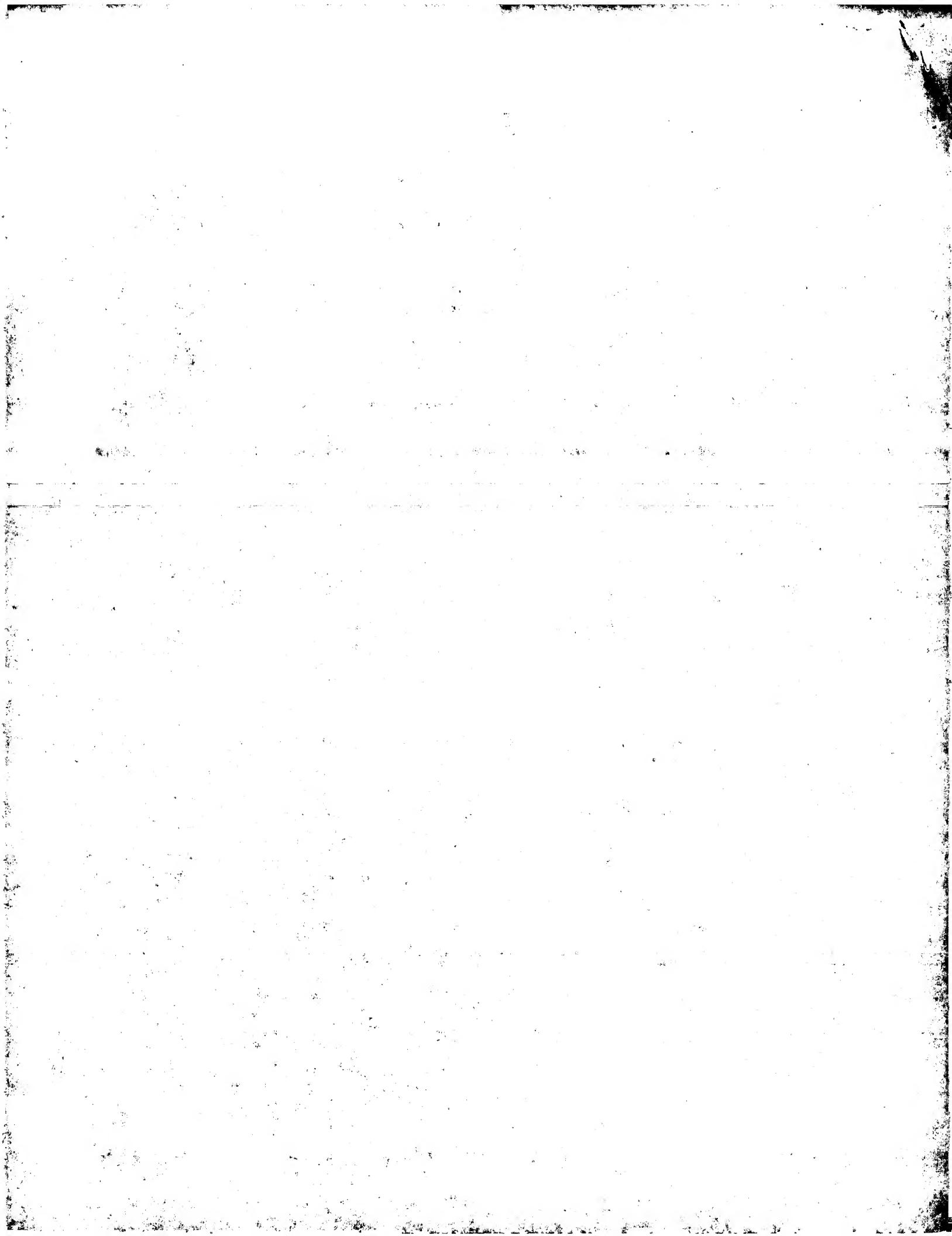
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ALIGMENTS

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; GENERAL INFORMATION:
; APPLICANT: Oligene Technologies, Inc
; TITLE OF INVENTION: BREAST CANCER TRANSCRIPTION FACTOR GENE AND USES
; FILE REFERENCE: 16U 107 R1
; CURRENT APPLICATION NUMBER: US/10/054,935
; CURRENT FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 4
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; TYPE: DNA
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; NAME/KEY: CDS
; LOCATION: (78)..(1922)
; OTHER INFORMATION:
US-10-054-935-1

Query Match 26.5%; Score 380.2; DB 1; length 4372;
Best Local Similarity 95.6%; Pred. No. 0; Mismatches 18; Indels 0; Gaps 0;
Matches 391; Conservative 0; MisMatches 18; Indels 0; Gaps 0;

Qy 331 GGAGGGGGTGGAGGGTAGACTCTACCCCATTTGAACTACAGAAAGAAGACTC 390



1 NAME_SEQUENCE 1.0
 LOCUS RSM80235 mRNA linear PRI 18-FEB-2000
 DEFINITION Homo sapiens mRNA; cDNA DKFZp586B1922 (from clone DKFZp586B1922).
 ACCESSION AL049450
 VERSION AL049450.1 GI:4500236
 KEYWORD SOURCE
 ORGANISM Homo sapiens (human)
 EUKARYOTA
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE AUTHORS
 1 (bases 1 to 1433) Koehrer, K., Bever, A., Meves, H. W., Gassenhuber, J. and Wiemann, S.
 TITLE JOURNAL
 Submitted (10-MAR-1999) MIFPS, Am Klopferspitz 18a, D-82152
 COMMENT
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
 This clone (DKFZp586B1922) is available at the RZPD, Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Chaillotzenburg, GERMANY. Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://www.mips.biochem.mpg.de/proj/cDNA/>.

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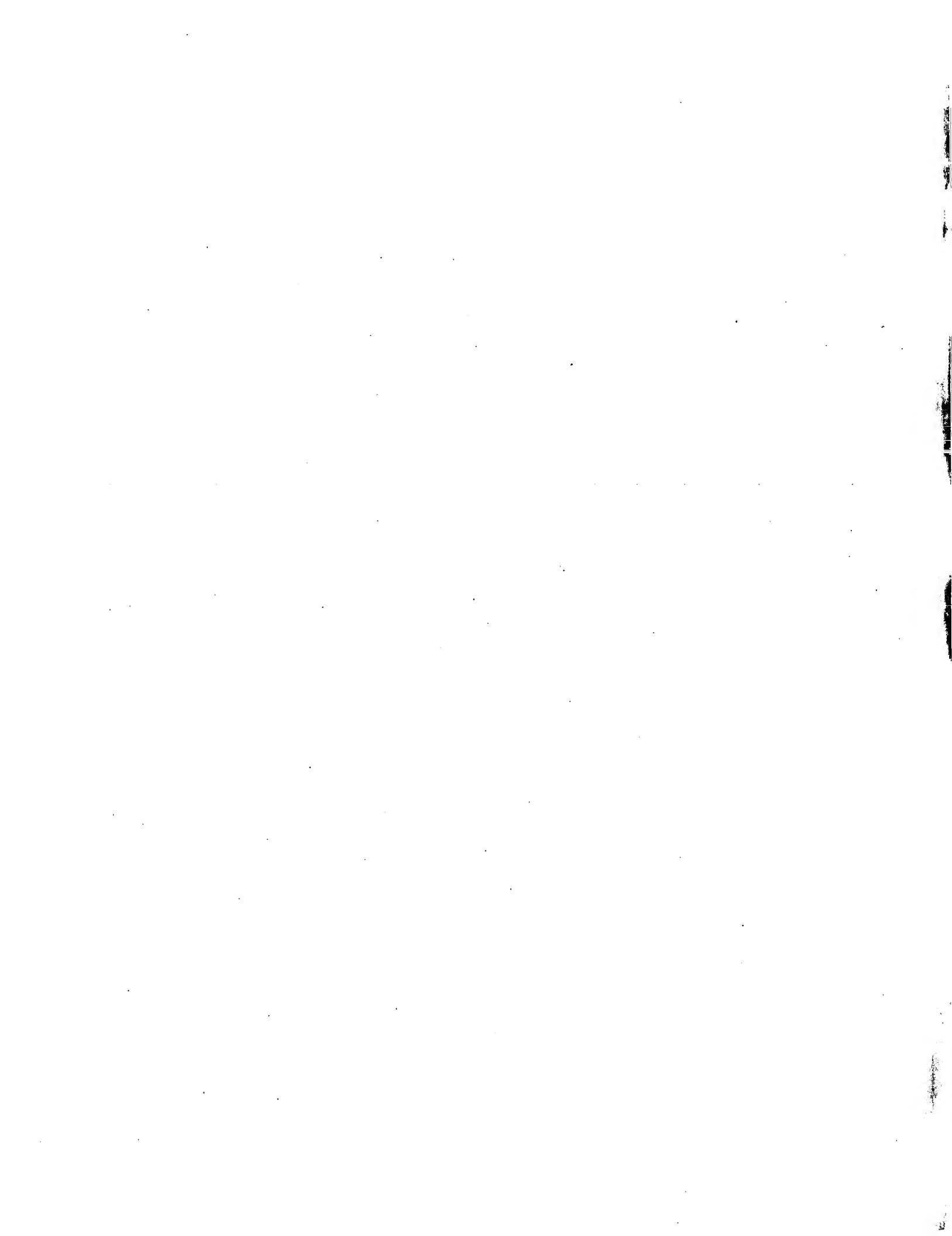
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(Without alignments)
4.177 Million cell updates/sec

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Searched: 1 seqs, 4372 residues

total number of MLEs satisfying chosen parameters.

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

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score greater than or equal to the s

and is derived by analysis of the total score distribution.

Result 8

ALIGNMENTS

RESULT 1
US-10-054-935-1
Sequence 1, Application US/10054935
GENERAL INFORMATION:
APPLICANT: OnGene Technologies, Inc.
TITLE OF INVENTION: BREAST CANCER TRANSCRIPTION FACTOR GENE AND USES
FILE REFERENCE: 16U 107 R1
CURRENT APPLICATION NUMBER: US/10/054-935
CURRENT FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 4372
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: CDS
NAME/KEY: CDS
LOCATION: (78)..(1922)
OTHER INFORMATION:
US-10-054-935-1

